

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: March 7, 2005, 07:04:17 ; Search time 31.7679 Seconds
(without alignments)
1193.323 Million cell updates/sec

Title: US-09-939-537-29_COPY_1_394
Perfect score: 2029
Sequence: 1 MNRGVPFRRLVLQLALP.....SGVLLSESNIKVLPMTSTPV 394

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 79: *
2: pir1: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2015	99.3	458	1 RWHUT4	T-cell surface gly
2	1867	92.0	432	1 RWC2T4	T-cell surface gly
3	1729	85.2	432	1 RWMQT4	T-cell surface gly
4	1146	56.5	459	2 A46254	CD4 precursor - ra
5	1099	54.2	432	2 S30193	T-cell surface gly
6	993	49.2	457	2 A27449	T-cell surface gly
7	983	48.9	457	1 RWMST4	T-cell surface gly
8	357	17.6	71	2 I60082	CD4 receptor - hum
9	305.5	15.1	99	2 S21461	T-cell surface gly
10	280.5	13.8	99	2 S21462	T-cell surface gly
11	162	8.0	739	2 JS0675	vascular cell adhe
12	155.5	7.7	538	2 JC2457	vascular cell adhe
13	155	7.6	739	2 A41288	vascular cell adhe
14	144	7.1	739	2 UN0581	vascular cell adhe
15	143	7.0	647	2 B41288	vascular cell adhe
16	138	6.8	398	2 I49443	gene 2B4 protein -
17	135	6.7	1259	2 S36126	neural cell adhesi
18	134.5	6.6	1260	1 S05479	neural cell adhesi
19	132	6.5	1011	2 T13669	neurotactin - fr
20	131.5	6.5	6831	2 A88852	protein unc-22 (im
21	131.5	6.5	6839	2 S57242	witchin [similari
22	131.5	6.5	7160	2 T27935	hypothetical prote
23	130.5	6.4	304	2 S04663	myosin-light-chain
24	130	6.4	1906	2 S68235	T-cell receptor ga
25	128	6.3	2783	2 T34416	hypothetical prote
26	127	6.3	2629	2 T32735	telomerase-associ
27	125.5	6.2	725	1 IJMSNG	neural cell adhesi
28	125	6.2	1447	2 A54100	tumor suppressor p
29	125	6.2	1896	2 T08851	Down syndrome cell

30	125	6.2	5175	2 T20992	hypothetical prote
31	125	6.2	5198	2 T43290	hemiscientin precurs
32	124	6.1	1115	1 IJMSNL	neural cell adhesi
33	124	6.1	7962	2 I38346	elastic titin - hu
34	123.5	6.1	323	2 S01895	T-cell receptor ga
35	123	6.1	4162	2 T42633	connectin/ctn - hu
36	122.5	6.0	761	1 IJHUNG	neural cell adhesi
37	122.5	6.0	1257	1 A41060	neural cell adhesi
38	121.5	6.0	338	2 JC4776	limbic-system-asso
39	121	6.0	946	2 S28061	SCP1 protein - rat
40	121	6.0	1091	1 IJCHNL	neural cell adhesi
41	121	6.0	1427	2 I51669	tumor suppressor -
42	120.5	5.9	333	2 A31923	amalgam protein pr
43	119.5	5.9	702	2 A36319	carcinoembryonic a
44	119	5.9	584	2 T06678	hypothetical prote
45	117	5.8	858	1 IJRTNC	neural cell adhesi

ALIGNMENTS

RESULT 1
RWHUT4
T-cell surface glycoprotein CD4 precursor [validated] - human
N/Alternate names: T-cell surface antigen T4/Les 3
C/Species: Homo sapiens (man)
C/Date: 28-May-1986 #sequence revision 31-Dec-1988 #text change 09-Jul-2004
C/Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039
R/Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, R.
Cell 42, 93-104, 1985
A/Title: The isolation and nucleotide sequence of a cDNA encoding the T cell surface prot
A/Reference number: A90872; NCBI:85254948; PMID:2990730
A/Accession: A90872
A/Molecule type: mRNA
A/Residues: 1-25, 'N', 27-458 <MAD>
A/Cross-references: UNIPROT:P01730
A/Experimental source: clone PT4B
R/Littman, D.R.; Maddon, P.J.; Axel, R.
Cell 55, 541, 1988
A/Title: Corrected CD4 sequence.
A/Reference number: A90907; NCBI:89028665; PMID:3263213
A/Contents: annotation; revision to residue 26
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A/Title: CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; NCBI:90182664; PMID:2107024
A/Accession: A32722
A/Status: nucleic acid sequence not shown; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 26-426, 428-458 <CAM>
R/Carr, S.A.; Henling, M.B.; Polena-Wasserman, G.; Sweet, R.W.; Anumula, K.; Barr, J.R.;
J. Biol. Chem. 264, 21286-21295, 1989
A/Title: Protein and carbohydrate structural analysis of a recombinant soluble CD4 recept
A/Reference number: A34194; NCBI:90078232; PMID:2592374
A/Contents: disulfide bonds; carbohydrate-binding sites
A/Accession: A34194
A/Molecule type: protein
A/Residues: 26-394 <CAR>
R/Lederman, S.; DeMartino, J.A.; Daugherty, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary, A.
Mol. Immunol. 28, 1171-1181, 1991
A/Title: A single amino acid substitution in a common African allele of the CD4 molecule
A/Reference number: A53287; NCBI:92072595; PMID:1961196
A/Accession: A53287
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 250-264, 'W', 266-280 <LED>
R/Bwards, M.C.; Gibbs, R.A.
Genomics 14, 590-597, 1992
A/Title: A human dimorphism resulting from loss of an Alu.
A/Reference number: I54176; NCBI:93052387; PMID:1330888
A/Accession: I54176
A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA
A/Reference number: 1-72 <RES>
A/Cross-references: GB:U47924; GB:M65525; GB:U72506; NID:gi633547; PIND:AA51309.1; PID:R.Hodge, T.W.; Sasso, D.R.; McDougal, J.S.
Hum. Immunol. 30, 99-104, 1991
A/Title: Humans with OKT4-epitope deficiency have a single nucleotide base change in the A/Reference number: 154297; MUID:91216786; PMID:1708753
A/Accession: 154297
A/Status: translated from GB/EMBL/DBD
A/Molecule type: DNA
A/Residues: 1-264, 'W', 266-458 <RE2>
A/Cross-references: GB:M35160; NID:gi79143; PIND:AA16069.1; PID:gi79144
A/Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine (C-C) receptor C/Genetics:
A/Status: GDB:CD4
A/Cross-references: GDB:119767; OMIM:186940
A/Map position: 12pter-12p12
A/Intons: 16/3
C/Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C/Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-458/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F:34-111/Domain: immunoglobulin homology <IM1>
F:136-186/Domain: immunoglobulin homology #status atypical <IM2>
F:216-299/Domain: immunoglobulin homology <IM3>
F:321-372/Domain: immunoglobulin homology <IM4>
F:397-420/Domain: transmembrane #status predicted <TM>
F:421-458/Domain: intracellular #status predicted <INT>
F:41-109,155-184,328-370/Dissulfide bonds: #status experimental
F:296,325/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.3%; Score 2015; DB 1; Length 458;
Best Local Similarity 99.5%; Pred. No. 9.5e-130;
Matches 392; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNRGVPRHLLVQLALIPATQGNKVVVGKKGTVEILTCTASQKKSIOFHMKNNOIK 60
DB 1 MNRGVPRHLLVQLALIPATQGNKVVVGKKGTVEILTCTASQKKSIOFHMKNNOIK 60
QY 61 IIGNQSFLTKGSKINDADSRSLMDQGNPLIKNKIIBSDPIYICVEVDQKEEVL 120
DB 61 IIGNQSFLTKGSKINDADSRSLMDQGNPLIKNKIIBSDPIYICVEVDQKEEVL 120
QY 121 LVFGLTANSDFHLLQGSITLTLESPPGSSPVQCSPPRGKNIQGGKITSVSLDELQDSG 180
DB 121 LVFGLTANSDFHLLQGSITLTLESPPGSSPVQCSPPRGKNIQGGKITSVSLDELQDSG 180
QY 121 LVFGLTANSDFHLLQGSITLTLESPPGSSPVQCSPPRGKNIQGGKITSVSLDELQDSG 180
DB 121 LVFGLTANSDFHLLQGSITLTLESPPGSSPVQCSPPRGKNIQGGKITSVSLDELQDSG 180
QY 181 TWCTVYLQNKKEFKIDIVLAFOKASSIVYKKEGEVFPFLAFVTEKLTGSGELMW 240
DB 181 TWCTVYLQNKKEFKIDIVLAFOKASSIVYKKEGEVFPFLAFVTEKLTGSGELMW 240
QY 241 QKERASSSWITPDLKKNKESVKKRYTODPKLOMGKKLPLHLTLPALPOYAGSGNLTLA 300
DB 241 QKERASSSWITPDLKKNKESVKKRYTODPKLOMGKKLPLHLTLPALPOYAGSGNLTLA 300
QY 301 LEAKTGKLEHVEVNLVVMRATOLQKNLTCEVWGFTSPKMLSLKLENKEAKVSKREKPVV 360
DB 301 LEAKTGKLEHVEVNLVVMRATOLQKNLTCEVWGFTSPKMLSLKLENKEAKVSKREKPVV 360
QY 361 LNPBAGMOCCLSDSGQVLLSNIKTLPTWSTPV 394
DB 361 LNPBAGMOCCLSDSGQVLLSNIKTLPTWSTPV 394

RESULT 2
RMC274
T-cell surface glycoprotein CD4 - chimpanzee
N/Alternate names: T-cell surface antigen T4/Len 3
C/Species: Pan troglodytes (chimpanzee)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: B32722; A46534
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990

A/Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; MUID:90182664; PMID:2107024
A/Accession: B32722
A/Molecule type: mRNA
A/Residues: 1-432 <CAM>
A/Cross-references: UNIPROT:P16004; GB:M31135
R/Fomsgaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
A/Title: Cloning and sequences of primate CD4 molecules: diversity of the cellular recept
A/Reference number: A46534; MUID:93049640; PMID:1425921
A/Accession: A46534
A/Status: not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 3-399 <ROM>
A/Note: sequence extracted from NCBI backbone (NCBIP:118332)
C/Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells t
C/Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C/Keywords: duplication; glycoprotein; T-cell; transmembrane protein
F:1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F:1-371/Domain: extracellular #status predicted <EXT>
F:8-86/Domain: immunoglobulin homology <IM1>
F:111-161/Domain: immunoglobulin homology #status atypical <IM2>
F:191-274/Domain: immunoglobulin homology <IM3>
F:296-347/Domain: immunoglobulin homology <IM4>
F:372-395/Domain: transmembrane #status predicted <TM>
F:396-432/Domain: intracellular #status predicted <INT>
F:16-84,130-159,303-345/Dissulfide bonds: #status predicted
F:271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 92.0%; Score 1867; DB 1; Length 432;
Best Local Similarity 98.6%; Pred. No. 1e-119;
Matches 363; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 27 KYVLGKKGTVEILTCTASQKKSIOFHMKNNOIKIIGNQSFLTKGSKINDADSRSL 86
DB 2 KYVLGKKGTVEILTCTASQKKSIOFHMKNNOIKIIGNQSFLTKGSKINDADSRSL 86
QY 87 MDQGNPLIKNKIIBSDPIYICVEVDQKEEVLVFGITANSDFHLLQGSITLTLES 146
DB 87 MDQGNPLIKNKIIBSDPIYICVEVDQKEEVLVFGITANSDFHLLQGSITLTLES 146
QY 62 WQGNFTLIIKNIKIEDSDPIYICVEVDQKEEVLVFGITANSDFHLLQGSITLTLES 121
DB 62 WQGNFTLIIKNIKIEDSDPIYICVEVDQKEEVLVFGITANSDFHLLQGSITLTLES 121
QY 147 PGSSPSVQCSPPRGKNIQGGKITSVSLDELQDSGVTCTVILQNKKEFKIDIVLAFOK 206
DB 147 PGSSPSVQCSPPRGKNIQGGKITSVSLDELQDSGVTCTVILQNKKEFKIDIVLAFOK 206
QY 122 PGSSPSVQCSPPRGKNIQGGKITSVSLDELQDSGVTCTVILQNKKEFKIDIVLAFOK 181
DB 122 PGSSPSVQCSPPRGKNIQGGKITSVSLDELQDSGVTCTVILQNKKEFKIDIVLAFOK 181
QY 207 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSSWITPDLKKNKESVKKR 266
DB 207 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSSWITPDLKKNKESVKKR 266
QY 182 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSSWITPDLKKNKESVKKR 241
DB 182 ASSIVYKKEGEVFPFLAFVTEKLTGSGELMWQKERASSSWITPDLKKNKESVKKR 241
QY 267 TDDPKLOMGKKLPLHLTLPALPOYAGSGNLTLAEAKTGKLEHVEVNLVVMRATOLQKNL 326
DB 267 TDDPKLOMGKKLPLHLTLPALPOYAGSGNLTLAEAKTGKLEHVEVNLVVMRATOLQKNL 326
QY 242 TDDPKLOMGKKLPLHLTLPALPOYAGSGNLTLAEAKTGKLEHVEVNLVVMRATOLQKNL 301
DB 242 TDDPKLOMGKKLPLHLTLPALPOYAGSGNLTLAEAKTGKLEHVEVNLVVMRATOLQKNL 301
QY 327 TCEVWGFTSPKMLSLKLENKEAKVSKREKPVVNLNPEAGMOCCLSDSGQVLLSNIK 386
DB 327 TCEVWGFTSPKMLSLKLENKEAKVSKREKPVVNLNPEAGMOCCLSDSGQVLLSNIK 386
QY 302 TCEVWGFTSPKMLSLKLENKEAKVSKREKPVVNLNPEAGMOCCLSDSGQVLLSNIK 361
DB 302 TCEVWGFTSPKMLSLKLENKEAKVSKREKPVVNLNPEAGMOCCLSDSGQVLLSNIK 361
QY 387 LPTWSTPV 394
DB 387 LPTWSTPV 394

RESULT 3
RMC274
T-cell surface glycoprotein CD4 - rhesus macaque
N/Alternate names: T-cell surface antigen T4/Len 3
C/Species: Macaca mulatta (rhesus macaque)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C/Accession: C32722
R/Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A/Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the vi
A/Reference number: A32722; MUID:90182664; PMID:2107024

A:Accession: C32722
 A:Molecule type: mRNA
 A:Residues: 1-432 <CAM>
 A:Cross-references: GB:M11134
 C:Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 C:Keywords: duplication; glycoprotein; T-cell; transmembrane protein
 F:1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MNT>
 F:1-371/Domain: extracellular #status predicted <EXT>
 F:9-86/Domain: immunoglobulin homology <IM1>
 F:111-161/Domain: immunoglobulin homology #status atypical <IM2>
 F:180-293/Domain: immunoglobulin homology <IM3>
 F:296-347/Domain: immunoglobulin homology <IM4>
 F:372-395/Domain: transmembrane #status predicted <TM1>
 F:396-432/Domain: intracellular #status predicted <INT>
 F:16-84,130-159,303-345/Disulfide bonds: #status predicted
 F:2771,300/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 85.2%; Score 1729; DB 1; Length 432;
 Best Local Similarity 90.8%; Pred. No. 2,6e-110;
 Matches 334; Conservative 16; Mismatches 18; Indels 0; Gaps 0;

QY 27 KVLGKGGDTVELTCTASQKSIQFHWKNSNOIKILGNQSPFLTKGSPKLNDRADSRRL 86
 DB 2 KVLGKGGDTVELTCTASQKNTQFHWKNSNOIKILGIQGLFLTKGSPKLSBRASRKL 61
 QY 87 WQGNPFLTIKMLKIEDSDTYICEVEDQEEVQLVFGLTANSDFHLQGSILTLTLESP 146
 DB 62 WQGGCSMTIHKMLKIEDSDTYICEVENKEEVELLVFGLTANSDFHLQGSILTLTLESP 121
 QY 147 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTCTVNLQNKKEFKIDIVVLAFOK 206
 DB 122 PSSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTCTVNLQNKKEFKIDIVVLAFOK 181
 QY 207 ASSIYKKEGQVRSFPPLAFVETKTGSGELLMQERASSSKSWITFPLKNEVSVKRV 266
 DB 182 ASSIYKKEGQVRSFPPLAFVETKTGSGELLMQERASSSKSWITFPLKNEVSVKRV 241
 QY 267 TDDPKLQMKKPLMLHTLQALPOVAGSGLTLTALFAKTKGKHQENVLVNMTATOLQKRL 326
 DB 242 TDDPKLQMKKPLMLHTLQALPOVAGSGLTLTALFAKTKGKHQENVLVNMTATOLQKRL 301
 QY 327 TCEVNGPTSPKMLSLKLENKAKVSKREKPVVNLNPEAGMOCILSDSGQVLLBSNIRV 386
 DB 302 TCEVNGPTSPKMLSLKLENKAKVSKREKPVVNLNPEAGMOCILSDSGQVLLBSNIRV 361
 QY 387 LPTWSTPV 394
 DB 362 VPTWPTPV 369

RESULT 4
 A46254
 C:Date: 21-Sep-1993 #sequence_cunicleus (domestic rabbit)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Accession: A46254
 R:Hague, B.F.; Sawadiksol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; Kindt, T.J.
 Proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
 A:Title: CD4 and its role in infection of rabbit cell lines by human immunodeficiency vi
 A:Reference number: A46254; MUID:92390370; PMID:1518821
 A:Accession: A46254
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-459 <HAG>
 A:Cross-references: UNIPROT:P46630; GB:M92840; NID:g164871; PIDN:AAA31198.1; PID:g164872
 A:Note: sequence extracted from NCBI backbone (NCBI:112732, NCBI:P:112733)
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 F:322-372/Domain: immunoglobulin homology <IM1>

Query Match 56.5%; Score 1146; DB 2; Length 459;
 Best Local Similarity 59.9%; Pred. No. 1,4e-70;
 Matches 236; Conservative 64; Mismatches 84; Indels 10; Gaps 5;

QY 1 NNRGVPEFRLTLVLQALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNOIK 60
 DB 1 NNRRIYFOCLLVLPLALLPATWTKTVRGKAGAVELPCQSSQKXNSVFMWKKANQVK 60
 QY 11GNQG---SFLTKGSPKLNDRADSRSLMDQGNPFLTIKMLKIEDSDTYICEVEDQEE 116
 DB 61 ILGNQSSSSSSFWLKNSPLSNRVSCKNMWQGSFPLTKDLRMDSDGTVICEVDKKN 120
 QY 117 EVQLVFGLTANSDFHLQGSILTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLEL 176
 DB 121 EVELLVFRITAPNPNRLHLQGSILTLTLESPVSGSPVQKSPENKILTEGPTCSMPKML 180
 QY 177 QDSGTCTV--NQNKKEFKIDIVVLAFOKASSIYKKEGQVRSFPPLAFVETKTGSG 235
 DB 181 QDSGTCTV--NQNKKEFKIDIVVLAFOKASSIYKKEGQVRSFPPLAFVETKTGSG 238
 QY 236 GELMMQERASSSKSWITFPLKNEVSVKRVTPDPLQMGKPLMLTLPOALPOVAGSG 295
 DB 239 GELMMQVDSASQSVWSFSLDRKVSQKILPDKIQMSKGLPLSLTLPOALHRYAGSG 298
 QY 296 NLTLALFAKTKGKHQENVLVNMTATOLQKNTCEVWGPSPKMLSLKLENKAKVSKRE 355
 DB 299 NLSLTLD--KGKLDQVSLVMLKVTQVKNKLTCEVAGPTDPKMLSLKLEDEKAVS--TQ 355
 QY 356 KPVVNLNPEAGMOCILSDSGQVLLBSNIRVPT 389
 DB 356 KVVQVLDPRKAGTMOCLISDGGQVLLBSKADVLAT 389

RESULT 5
 S30193
 T-cell surface glycoprotein CD4 - dog
 C:Species: Canis lupus familiaris (dog)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jul-2000
 C:Accession: S30193
 R:Milde, K.F.; Comer, G.B.; Mintz, D.H.; Alejandro, R.
 Biochim. Biophys. Acta 1172, 315-318, 1993
 A:Title: Primary structure of the canine CD4 antigen.
 A:Reference number: S30193; MUID:93192324; PMID:7916632
 A:Accession: S30193
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-432 <MLT>
 A:Cross-references: EMBL:X68865; NID:g288652; PIDN:CA37664.1; PID:g4467377
 C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
 F:202-311/Domain: immunoglobulin homology <IM1>

Query Match 54.2%; Score 1099; DB 2; Length 432;
 Best Local Similarity 57.7%; Pred. No. 2e-67; Mismatches 86; Indels 18; Gaps 6;
 Matches 226; Conservative 62; Mismatches 86; Indels 18; Gaps 6;

QY 12 LVLQALPAAQGNKVVLGKKGDTVELTCTASQKSIQFHWKNSNOIKILGNQSPFLTK 71
 DB 1 LMLQVLMPLAVPVAREVVLGKGAVALPCQSSQKNIHNMWDSMWQILGNQSPFTV 60
 QY 72 GPKLNDRADSRSLMDQGNPFLTIKMLKIEDSDTYICEVEDQEEVQLVFGTLA---- 127
 DB 61 GSSRLKHRVSKKNLMDQGSFPLVTKDLVADSGYFCDT-DKROBEVELLVNLTAKMDS 119
 QY 128 -----NSDTHLQGSILTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTW 182
 DB 120 GSSGSSNIRLQGGQTLTLTLESPSSPVQCRSPRGKNIQGGKTLVSQLELQDSGTW 179
 QY 183 TCTVNLQNKKEFKIDIVVLAFOKASSIYKKEGQVRSFPPLAFVETKTGSGELMMQ 242
 DB 180 TCTVNLQNKKEFKIDIVVLAFOKASSIYKKEGQVRSFPPLAFVETKTGSGELMMQ 237
 QY 243 ERASSSKSWITFPLKNEVSVKRVTPDPLQMGKPLMLTLPOALPOVAGSGNTLALF 302
 DB 238 QDASSSLWISFTLENRKLSMKEAHAPKLOMKESLPLRFTLPVLSRYAGSGILTLNL- 296

Matches 211; Conservative 62; Mismatches 109; Indels 10; Gaps 7;

QY 1 MNRGVPFRPH-LLVLTQALLPAATQGNKVLTGKGGDTVELTCTASQKKSIOFPHKANSNOI 59
Db 1 MCRATSLRRLLLLLOLSQALLAVTQKTLVVGKGESEALPCBESSOKKITVFTWKFSDBR 60

QY 60 KILINOG-SFLTKG--PSKLNDRADSRRLSDQGNFPLIINKLIEPDSDFYICEVEDPCKE 116
Db 61 KILQOHGKGVILIRGGSFSQF-DREFDSKKAMEKSPFLIINKLMEDSOYICLENRKE 119

QY 117 EVOLLVEGLTANSDTHLLOGSLTLTLDES-PRGSSPSVOCSPRGKNOIGGKTLVSQLE 175
Db 120 EVELMVFVKVTPSPGSHLLQGGSLTLTLDSNSKVSNPFLTECHGKKGKVVSGSKVLSMENLR 179

QY 176 LODSGTCTCTVLTQNOQKVEFKIDIVLAFQCAASSIVYKKEGQVPEFSPPLAFYTEKLTGS 235
Db 180 VQDSDFNNCTVTLTQCKKMFGMTLSVLGFQSTATAYKSEESAEFSPPLFAER--NGW 237

QY 236 GELMWOAEBSASSSWITPDLKKNKEVSKRATODPKQMGKCLPLHLTLPOALPOVAGSG 295
Db 238 GELMWOAEBSASSSWITPDLKKNKEVSKRATODPKQMGKCLPLHLTLPOALPOVAGSG 297

QY 296 NLTLALEAKTQKTLQEQEVLVYMRATOLQKNTLCVWGSPSPKMLSLKLENKAESKRE 355
Db 298 NLTLTLTD-KETLQHEVNLVYMKVAQLNNTLTCEVMGTPSRKMLTLKQENGEARVSEEQ 355

QY 356 KPVAVLNPEAGMWOCCLSDSGVLLSESNIKYL 387
Db 356 KVVQVVAPEGTGLMOCCLSEGDVKVMDSRIVL 387

RESULT 8

CD4 receptor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I60082

R:Zverev, V.V.; Sidorov, A.V.; Nedospasov, S.A.; Malinshova, V.V.; Udalova, I.A.; Andzhana
Vopr. Vkrusol. 40, 100-102, 1995
A:Title: [Nucleotide sequence of two exons of the human T-lymphocyte CD4 receptor gene].
A:Reference number: I60082; MUID:95407135; PMID:766667
A:Accession: I60082
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-71 <RES>
A:Cross-references: UNIPROT:Q13969; GB:S79267; NID:g1086922; PIRN:AA835273.1; PID:g1086922
C:Genetics:
A:Introns: 17/1
C:Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology

Query Match 17.6%; Score 357; DB 2; Length 71;
Best Local Similarity 98.6%; Pred. No. 6.5e-18;
Matches 70; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNRGVPFRPHLLVLTQALLPAATQGNKVLTGKGGDTVELTCTASQKKSIOFPHKANSNOIK 60
Db 1 MNRGVPFRPHLLVLTQALLPAATQGNKVLTGKGGDTVELTCTASQKKSIOFPHKANSNOIK 60

QY 61 ILGNQGSFLTK 71
Db 61 ILGNQGSFLTK 71

RESULT 9

S21461
T-cell surface glycoprotein CD4 (allele 1) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: I47131; S21461
R:Guetafesson, K.; Germania, S.; Sundt, T.M.
J. Immunol. 151, 1365-1370, 1993
A:Title: Extensive allelic polymorphism in the CDR2-like region of the miniature swine C

Reference number: I47131; MUID:95329116; PMID:8355933

A:Accession: I47131
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule/type: mRNA
A:Residues: 1-99 <GU2>
A:Cross-references: UNIPROT:Q29027; EMBL:X65629; NID:g1928; PIDs:CAA46583.1; PID:g388232
C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
C:Keywords: glycoprotein; T-cell
F:3-81/Domain: immunoglobulin homology <IMM>

Query Match 15.1%; Score 305.5; DB 2; Length 99;
Best Local Similarity 60.2%; Pred. No. 3.2e-14;
Matches 59; Conservative 16; Mismatches 22; Indels 1; Gaps 1;

Oy 32 KKGDVETLTCTASOKKSIOFHWNKSNQIKILGNQSFLTKGP-SKLNDRADRSRLMDQG 90
 ||| |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 1 KAGDIAELPCHSSÖKKNLPEFMNKNSTQTKILGSHGSWMHTASVELTSRLDSKKMMWDHG 60
 ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

Oy 91 NFPLIIKNLIKEDSDTYICEVEDQKEEVOLLVGLTAN 128
 :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 61 SFPLIINKLEVTDSGIYICEVEDKRILEVOLLVRLTAS 98
 :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

RESULT 10

S21462
T-cell surface glycoprotein CD4 (allele 2) - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C:Accession: I47132; S21462
R:Guatafason, K.; Germana, S.; Sundt, T.M.
J:Immunol. 151, 1365-1370, 1993
A>Title: Extensive allelic polymorphism in the CD82-like region of the miniature swine C
A:Reference number: I47131; MWID:93329116; PMID:8335933
A:Accession: I47132
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-99 <GU2>
A:Cross-references: UNIPROT:Q29028; EMBL:X65630; NID:g1929; PIDs:CAA46584.1; PID:g388233
C:Superfamily: T-cell surface glycoprotein CD4; Immunoglobulin homology
C:Keywords: glycoprotein; T-cell
F:3-81/Domain: immunoglobulin homology <IMM>

Query Match 13.8%; Score 280.5; DB 2; Length 99;
Best Local Similarity 56.1%; Pred. No. 1.6e-12;
Matches 55; Conservative 19; Mismatches 23; Indels 1; Gaps 1;

Oy 32 KKGDVETLTCTASOKKSIOFHWNKSNQIKILGNQSFLTKGP-SKLNDRADRSRLMDQG 90
 ||| |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 1 KAGDIAELPCHSSÖKKNLPEFMNKNSTQTKILGRHRNMHTASVELTSRLDSKKMMWDHG 60
 ::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

Oy 91 NFPLIIKNLIKEDSDTYICEVEDQKEEVOLLVGLTAN 128
 :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 61 SFPLIINKLEVTDSGIYICEVEDKRILEVOLLVRLTAS 98
 :|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:

RESULT 11

J50675
vascular cell adhesion molecule-1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: J50675; S19872; S23136
R:Hesslein, C.; Moy, P.; Tizad, R.; Chisholm, P.; Williams, C.; Wisk, M.; Burki, L.; Mi
Biochem. Biophys. Res. Commun. 183, 163-169, 1992
A>Title: Cloning of murine and rat vascular cell adhesion molecule-1.
A:Reference number: J50674; MWID:92181437; PMID:1371918
A:Accession: J50675
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-739 <HES>
A:Cross-references: UNIPROT:D29314; GB:W84488; NID:g207642; PIDs:AAA42332.1; PID:g207643
R:Williams, A.; Atkins, R.; Fries, J.; Gimprone, M.A.; Cybulsky, M.I.; Collins, T.
submitted to the EMBL Data Library, February 1992
A>Description: Nucleotide sequence of rat vascular cell adhesion molecule-1.
A:Reference number: S19872

A/Accession: S19872
 A/Molecule type: mRNA
 A/Residues: 1-2, 'G', '4-121, 'HL', 124-165, 'N', 167-738, 'G' <W1>
 A/Cross-references: EMBL:X63722; NID:g57471; PIDD:CAA5254.1; PID:g57472
 R/Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.; Colla
 R/Biochem. Biophys. Acta 1131, 214-216, 1992
 A/Title: Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.
 A/Reference number: S23136; MUID:92305064; PMID:1377031
 A/Accession: S23136
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-2, 'G', '4-165, 'N', 167-738, 'G' <W2>
 C/Comment: This protein interacts with the beta-1 integrin very late antigen 4 on leukoc
 C/Genetics:
 A/Genes: VCAM-1
 C/Keywords: cell adhesion; transmembrane protein
 F/1-24/Domain: signal sequence #status predicted <SIG>
 F/25-739/Product: vascular cell adhesion molecule 1 #status predicted <VAS>
 F/239-293/Domain: immunoglobulin homology <IMM1>
 F/328-385/Domain: immunoglobulin homology <IMM2>
 F/526-581/Domain: immunoglobulin homology <IMM3>
 F/676-696/Domain: transmembrane #status predicted <TRA>
 F/697-715/Domain: intracellular #status predicted <INT>

Query Match 8.0%; Score 162; DB 2; Length 739;
 Best Local Similarity 22.0%; Pred. No. 0.0024;
 Matches 86; Conservative 60; Mismatches 155; Indels 90; Gaps 14;

QY 33 KGDVLTCTAGSKSIQFHWNKSNQIKILGNQSLTGTGPKSLNDRADSRSLMDQGNF 92
 DB 238 EGAATVMTCASEGTPAPRIFFMSKK-----LDNGVQLL-----SGNA 274
 QY 93 PLIKNLKIEDSDTYICE---VEDQKEVQLLV-----FGLTANSDTHLLQGQSLTLT 142
 DB 275 TLTLAMREDESDGIYCEGVNLVGRKTVELLVQKRPVTDISPSQVAQVDSVULT 334
 QY 143 LESPSSSPSVQCRSPRGKNIQ-----GKTLVSQLELDQSGTWCTVTLQNKRVF 195
 DB 335 CAVGCDSFSPFWRQTQDSPLNGEVDEGATSTLTLSPGVEDEHSYLCVTTCQRKLEK 394
 QY 196 KIDIVLAQOKXASIVYKKEGQVEFSFPLA-----FIVEKLTGSG 236
 DB 395 TLQVEYYSF-----PEDEPIETISGLVHGRPVTVNCTVPNVYRPFHLLEILKGET 445
 QY 237 ELWMQAEKAS-SKSWITFDLKNKEVSVKRVTDPTQLQMGKTL---PLHLLPQLP-Q 290
 DB 446 TLNKLRLREIGTKS---LETSLEMTFIPFAD-----TGKALVCLAKLHSSQMESEPKQ 498
 QY 291 VAGSGNLTALBAKTKGLHGVNLVVMRAVTLQKNITCEVWGPTSPKMLSLKLENKAK 350
 DB 499 ROSTQTLVYNVAPKEPTIVWSPPVPEEGSPV--NLTCSSDGFPPPKILMSRQLKNGELQ 556
 QY 351 VSKREKPVAVLNPEAGMOCCLSDSQVLL 381
 DB 557 PLISQ-----NTTISFMATKMEISGIVCE 580

RESULT 12

vascular cell adhesion protein - pig
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 15-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
 A/Accession: J02457
 R/Tsang, Y.T.M.; Haskard, D.O.; Robinson, M.K.
 A/Title: Cloning and expression kinetics of porcine vascular cell adhesion molecule.
 A/Reference number: J02457; MUID:94271236; PMID:7516159
 A/Accession: J02457
 A/Molecule type: mRNA
 A/Residues: 1-538 <TSA>
 A/Cross-references: UNIPROT:028939; EMBL:U08351; NID:g474382; PIDD:AAA21542.1; PID:g4743
 C/Keywords: glycoprotein; transmembrane protein
 F/497-517/Domain: transmembrane #status predicted <TM>

F/75,157,271,330,360/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 7.7%; Score 155.5; DB 2; Length 538;
 Best Local Similarity 23.4%; Pred. No. 0.0045;
 Matches 65; Conservative 49; Mismatches 91; Indels 73; Gaps 11;

QY 32 KKDVTLELTCTAGSKSIQFHWNKSNQIKILGNQSLTGTGPKSLNDRADSRSLMDQGN 91
 DB 235 QEGDSMMMTCTSEGAPAPQISW-----SKLDNDQQLL-----SGN 271
 QY 92 PPLIKNLKIEDSDTYICE---VEDQKEVQLLV-----FGLTANSDTHLLQGQSLTL 141
 DB 272 ATLTLIAMREDESDGIYCEGVNLVGRKTVELLVQKRPVTDISPSQVAQVDSVULT 331
 QY 142 TLESPSSSPSV-----QCRSPRGKNIQSGKTLVSQLELDQSGTWCTVTLQ-----NOKRV 193
 DB 332 TCSSGFPAPKTLWKKKLDGNLPLSENTVTLTLSTYKMEDESDGIYCEGVNLVGRKTV 391
 QY 194 EFKI-----DIVLAQOKXAS-----SIYKKE-----GEQVEFSFPLA 226
 DB 392 ELILQAPKIDQTLTFPSESVEKSDPTVLIISCTGVNPPVTLILKKKAEHGTVLKSTDGA 451
 QY 227 FIVEKLT-----TSGGELWMQAEKASIKWITFDLKNKE 260
 DB 452 YTHRARLADAGVCEKSKNETGLQLRG-ITLDVKGRE 488

RESULT 13

vascular cell adhesion molecule 1, long splice form precursor - human
 A/Accession: A41288
 N/Alternate names: VCAM-1
 C/Species: Homo sapiens (man)
 C/Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004
 A/Accession: A41288; S11476; A39755; B39755; A61160; A4352; PH1379; A39554
 R/Cybulsky, M.I.; Fries, J.W.U.; Williams, A.J.; Sultan, P.; Eddy, R.; Byers, M.; Shows,
 Proc. Natl. Acad. Sci. U.S.A. 88, 7859-7863, 1991
 A/Title: Gene structure, chromosomal location, and basis for alternative mRNA splicing of
 A/Reference number: A41288; MUID:91352090; PMID:1715583
 A/Accession: A41288
 A/Molecule type: DNA
 A/Residues: 1-739 <CYB>
 A/Cross-references: UNIPROT:P19320; GB:M73255; NID:g340195; PIDD:AAA61270.1; PID:g340196
 R/Polte, T.; Newman, W.; Gopal, T.V.
 Nucleic Acids Res. 18, 5901, 1990
 A/Title: Full length vascular cell adhesion molecule 1 (VCAM-1).
 A/Reference number: S11476; MUID:91016951; PMID:1699207
 A/Accession: S11476
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-739 <POL>
 A/Cross-references: EMBL:X53051; NID:g37648; PIDD:CAA37218.1; PID:g37649
 R/Hession, C.; Tizard, R.; Vassallo, C.; Schiffer, S.B.; Goff, D.; Moy, P.; Chi-Rosso, G.
 J. Biol. Chem. 266, 6682-6685, 1991
 A/Title: Cloning of an alternate form of vascular cell adhesion molecule-1 (VCAM1).
 A/Reference number: A39755; MUID:91201302; PMID:1707873
 A/Accession: A39755
 A/Status: nucleic acid sequence not shown
 A/Molecule type: mRNA
 A/Residues: 25-646, 648-739 <HEB1>
 A/Cross-references: GB:M60335
 A/Note: the complete translation is not shown
 A/Accession: B39755
 A/Status: not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-739 <HEB2>
 A/Cross-references: GB:M60335; NID:g340193; PIDD:AAA61269.1; PID:g340194
 R/Cybulsky, M.I.; Fries, J.W.U.; Williams, A.J.; Sultan, P.; Davis, V.M.; Gimbrone Jr., P.
 Am. J. Pathol. 138, 815-820, 1991
 A/Title: Rapid communication. Alternative splicing of human VCAM-1 in activated vascular
 A/Reference number: A61160; MUID:91189297; PMID:1707234
 A/Accession: A61160
 A/Status: not compared with conceptual translation

A: Molecule type: mRNA
 A: Residues: 25-401, 'T', 403-686 <CY2>
 R: Iademaeco, M.P.; McQuillan, J.J.; Rosen, G.D.; Dean, D.C.
 J. Biol. Chem. 267, 16323-16329, 1992
 A: Title: Characterization of the promoter for vascular cell adhesion molecule-1 (VCAM-1)
 A: Reference number: A43352; MUID:92355594; PMID:1379595
 A: Accession: A43352
 A: Molecule type: DNA
 A: Residues: 1-21 <TAD>
 A: Cross-references: GB:M92431; NID:9340197
 A: Note: sequence extracted from NCBI backbone (NCBIN:110680, NCBIPI:110681)
 R: Osborn, L.; Vassallo, C.; Benjamin, C.D.
 J. Exp. Med. 176, 99-107, 1992
 A: Title: Activated endothelium binds lymphocytes through a novel binding site in the alpha
 A: Reference number: PH1379; MUID:92308660; PMID:1377228
 A: Accession: PH1379
 A: Molecule type: protein
 A: Residues: 25-181, 'G', 183-402 <OSB>
 C: Comment: This adhesion molecule is induced on endothelial cells by inflammatory cytokines
 C: Genetics:
 A: Gene: GDB:VCAM1
 A: Cross-references: GDB:127922; OMIM:192225
 A: Map position: 1p32-1p31
 C: Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-739/Product: vascular cell adhesion molecule 1, long splice form #status predicted
 F: 25-698/Domain: extracellular #status predicted <EXT>
 F: 699-720/Domain: transmembrane #status predicted <TM>
 F: 721-739/Domain: intracellular #status predicted <INT>
 F: 273,365,417,463,531,561/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.6%; Score 155; DB 2; Length 739;
 Best Local Similarity 21.9%; Pred. No. 0.0073;
 Matches 91; Conservative 71; Mismatches 166; Indels 88; Gaps 18;

8 RHLLVQLALPAAT--OGNRVVLGKKDYLCTASQKSIOPHWKNSQIKILNQ 65
 211 RQAVKELQYISPKNTVISVNPSTKLQEGSVTMTCSSEGLPAPEIFW----- 258
 QY
 66 GSFLTKGSPKLNDRADSRSLMDQGNFPIIKLKIKEDSDTYICE---VEDQKEVQL 121
 259 -----SKKLDNGNLQHL---SGNATLTLLAMRREDGIIYCEGVNLIGKRKKEVELI 307
 DB
 122 V----FGLTANSPTHLIQ--GOSLTTLTLESPPGSSPVQCRSPRGNIQ-----GKT 168
 308 VQEKPFYVETISGPRIAQIGSWLTCVWGCESSFSFWRTOIDSPLSGKVRSEGTNST 367
 QY
 169 LSVQLELDQSGTWTCTVLQNOQKVEFKIDIVLAFQKASIVYK---KEGROVERF--- 222
 368 LTLSPVSPFENHSYLCVTYCGHKLEKGLQVELYSFRPDPEIEMSGLVNGSSVTYSCKV 427
 DB
 223 ---PPL-AFTVEKLTGSGELMWOAERASSKSKITF---DLKNEVSVKRYTODPKLO- 273
 428 PSVYPLRLLEILDKGETIL-----ENIEFLBDTDMKSLKNSKLEMTFPIPTID 476
 QY
 274 WKKK----PLHLTLPLQALPOYAGSGNTLALAEKTKGLHGVNVLVMAATQLOK-----N 325
 477 TKALAVCOAKLHIDMEFEPKQROF---TQTLVNVAP--RDTTVLVASSSTILESSSVN 531
 DB
 326 LITCEVWGSPSPKMLSLKLENKAKVSKREKPPVVLNPEAGMWOCLSSDGVLTLE 381
 532 WTCLSGFPAPKILMRSQPLNGELOPLSENATITLSTK-----MEPSGVYLCE 580

RESULT 14
 JN0581
 vascular cell adhesion molecule-1 long splice form precursor - mouse
 C: Species: Mus musculus (house mouse)
 C: Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
 C: Accession: JN0581; US0674; A40275; A48919
 R: Araki, M.; Araki, K.; Vassalli, P.
 Gene 126, 261-264, 1993
 A: Title: Cloning and sequencing of mouse VCAM-1 cDNA.

A: Reference number: JN0581; MUID:93246254; PMID:7683304
 A: Accession: JN0581
 A: Molecule type: mRNA
 A: Residues: 1-739 <ARA>
 A: Cross-references: UNIPROT:P29533; EMBL:X67783; NID:9298116; PID:CA47989.1; PID:929811
 R: Hession, C.; Moy, P.; Tizad, R.; Chisholm, P.; Williams, C.; Wyse, M.; Burki, L.; Mij
 Biochem. Biophys. Res. Commun. 183, 163-169, 1992
 A: Title: Cloning of murine and rat vascular cell adhesion molecule-1.
 A: Reference number: J50674; MUID:92181437; PMID:1371918
 A: Accession: J50674
 A: Status: nucleic acid sequence not shown
 A: Molecule type: mRNA
 A: Residues: 1-739 <HES>
 A: Cross-references: GB:M84487; NID:9202345; PID:AAA40545.1; PID:9202346
 R: Miyake, K.; Medina, K.; Ishihara, K.; Kimoto, M.; Auerbach, R.; Kincaid, P.W.
 J. Cell Biol. 114, 557-565, 1991
 A: Title: A VCAM-like adhesion molecule on murine bone marrow stromal cells mediates bindi
 A: Reference number: A40275; MUID:91317872; PMID:1715392
 A: Accession: A40275
 A: Molecule type: protein
 A: Residues: 'XX', 27-32 <MTY>
 R: Cybulsky, M.I.; Allan-McMamed, M.; Collins, T.
 Genomics 18, 387-391, 1993
 A: Title: Structure of the murine VCAM1 gene.
 A: Reference number: A48919; MUID:94117008; PMID:7507076
 A: Accession: A48919
 A: Molecule type: DNA
 A: Residues: 1-692, 'N', 694-739 <CYB>
 A: Cross-references: GB:L22353; NID:9347981; PID:AAA16921.1; PID:9459893; GB:L22301
 C: Comment: This protein is a transmembrane protein and interacts with the beta-1 integrin
 C: Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
 F: 1-24/Domain: signal sequence #status predicted <SIG>
 F: 25-739/Product: vascular cell adhesion protein-1 #status predicted <MAT>
 F: 239-292/Domain: immunoglobulin homology <IMW1>
 F: 328-385/Domain: immunoglobulin homology <IMW2>
 F: 527-581/Domain: immunoglobulin homology <IMW3>
 F: 699-720/Domain: transmembrane #status predicted <TM>
 F: 225,273,424,531,561/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.1%; Score 144; DB 2; Length 739;
 Best Local Similarity 20.2%; Pred. No. 0.041;
 Matches 79; Conservative 65; Mismatches 147; Indels 100; Gaps 15;

32 KKGDYVELTCTASQKSIOPHW--KNSNQI-KILNGSGFLTKGSPKLNDRADSRSLMD 88
 237 QEGGAVTMTCSSEGLPAPEIFGKRLDNEVQLL----- 270
 QY
 89 QGNFPIIKLKIKEDSDTYICE---VEDQKEVQLV-----FGLTANSPTHLIQGOS 138
 271 SGNATLTLLAMRREDGIIYCEGVNLIGRDKALEVELVQEKPFYVIDISPGSVAAQVGD 330
 DB
 139 LTLTLESPPGSSPVQCRSPRGNIQ-----GKTLVSQLELDQSGTWTCTVLQNOQ 191
 331 VVLTCAATGCDSPSPSWRQTQDSPINGVRNAGASTVLSSVGEDEHSYLCATVCLQR 390
 QY
 192 KYEFPKIDIVLAFQKASIVYKKEGROVERFSPPLA-----FTVEKYL 232
 391 TLEKTIQVEVYF-----PEDPVIMSGPLVHGRPVYVNCVYVPPDHLIELL 441
 DB
 233 TSGSGELMWOAERASSKSWI--TFDLKNEVSVKRYTODPKLO--MGKTL---PLHLTLQ 286
 442 KG-----FTLTKKRYVLEMGIKSLKLETKLLETFPIPTIDTGSLVCLARLHSGWE 493
 QY
 287 ALPOYAGSGNTLALAEKTKGLHGVNVLVMAATQLOK-----NLNCEVWGSPSPKMLSL 342
 494 SEPKQROFQPLVNVAP-----KETTIVWSPSPILEBSSPVNLTCSSDGIAPKILMSR 548
 DB
 343 KLENKAKVSKREKPPVVLN--PEAGMWO 370
 549 QLNAGELQPLSENTITLTFTWSTRDSDGIYVC 579

RESULT 15

B41288
vascular cell adhesion molecule 1, short splice form precursor - human
N:Alternate names: VCAM-1
C:Species: Homo sapiens (man)
C>Date: 03-Apr-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C/Accession: B41288; A33758
R:Cybulsky, M.I.; Fries, J.W.U.; Williams, A.V.; Sultan, P.; Eddy, R.; Byers, M.; Shows, Proc. Natl. Acad. Sci. U.S.A. 88, 7859-7863, 1991
A>Title: Gene structure, chromosomal location, and basis for alternative mRNA splicing
A:Reference number: A41288; MUID:91552090; PMID:1715583
A:Accession: B41288
A:Molecule type: DNA
A:Residues: 1-647 <CYB>
A:Cross-references: UNIPROT:P19320; GB:M73255
R:Osborn, L.; Hession, C.; Tizard, R.; Vassallo, C.; Lubowsky, S.; Chi-Rosso, G.; Lobb, Cell 59, 1203-1211, 1989
A>Title: Direct expression cloning of vascular cell adhesion molecule 1, a cytokine-indu
A:Reference number: A33758; MUID:90090619; PMID:2688898
A:Accession: A33758
A:Molecule type: mRNA
A:Residues: 1-647 <OSB>
A:Cross-references: GB:M30257; NID:g179885; PIDN:AA51917.1; PID:g179886
C:Keywords: alternative splicing; cell adhesion; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <Sig>
F:25-647/Product: vascular cell adhesion molecule 1, short form #status predicted <MAT>
F:25-606/Domain: extracellular #status predicted <EXT>
F:607-628/Domain: transmembrane #status predicted <TM>
F:629-647/Domain: intracellular #status predicted <INT>
F:273,325,371,439,469/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 143; DB 2; Length 647;
Best Local Similarity 20.9%; Pred. No. 0.04;
Matches 105; Conservative 81; Mismatches 151; Indels 166; Gaps 25;

QY 16 LALLPAATGKNV-----VLGKGDYBELCTASQKSIQFMKNSQIKLG---NQ 65
DB 15 LMIWPAASQAFKIEETTPESRYLAQIGDSVLTCTGCSPPFSWRTQIDSPINGKVTNE 74
QY 66 G--SFLTKGPKSLNDR-----ADSRSLWDOG-----NFP----- 93
DB 75 GTTSTLTNNPVSFGNHSYLTCTATCESRK--LEKGIQVEIYSPFKDPEIHLGPLEAGKP 132
QY 94 -----LIIKNLK-----IEDSD-----TYICEVED--- 113
DB 133 ITVKCSVADVPPDRLEIDLKGDHLKMSQEFLEADRSLETSLLEVFTFVIEDIGKV 192
QY 114 -----QKEVQLVFG-----LTANSDTHLQGSLLTTLBSPPGS 149
DB 193 LVCRAKLHIDEMDSVPTVROAVKELOVYISPRNTVIVSVPSTKLQGGSVTWTCSSEGLP 252
QY 150 SPSV-----QCRSPRGKNIQGGKTLISVSOLELQDSGTWTC---TVLONOKVEFKIDIV 201
DB 253 APEIFWMSKLDNGNQHLSGNNTLITLIARMEDSGIYCEGNILGNKRYE----LIV 308
QY 202 LAFQKASSIVYK--KEGEQVEFS-----FPL-AFTVEKLTGSGELMWQABRASSSKSW 251
DB 309 QAFPRDPRIEMSGGLVNGSSVTVSCVPSVYPLDLRIEILKGETIL-----EN 357
QY 252 ITF-----DLKNKEVAVKRTQDPKQ--MGKCL-----PLHLTPQALPOYAGSNLTIALE 302
DB 358 IEFLEDTDMKSLKNSLEMTPIPTLEDTEKALVCOAKLHIDMEPEPKORQ--TOTLY 414
QY 303 AKTGKIHQEVNLVVMRATQLOK---NLTCENVGPTSPKMLSLKLENKAKVSKREKPV 358
DB 415 VNVAV--RDTTYLVBPSSILBEGSSVNMTCLSQGFPAKILMSRQLPNGELOPLSENATL 472
QY 359 WVLNPEAGMWCCLSDSQVLLR 381
DB 473 TLISTK-----MEDSGVYLCE 488